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GeneChip Array Information

Probe Set ID M64347_at
GeneChip Array HumanGeneFL Array
Organism Common Name Human

Probe Design Information

Transcript ID M64347
Sequence Type Exemplar sequence
Representative Public ID M64347 [NCBI](#)
Target Description M64347, class A, 20 probes, 20 in M64347 3336-3720, Human novel growth factor receptor mRNA, 3' cds

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)

Alignment(s)	Position	% Identity	Cytoband
chr4: 1771773-1772182 (+) UCSC	93	p16.3	

	Representative Transcript	UniGene Description	Position
Overlapping Transcripts	NM_000142 NCBI	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	chr4:1757261-1772237 (+) UCSC
	NM_022965 NCBI	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	chr4:1757261-1772237 (+) UCSC

Public Domain and Genome References

Gene Title fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
Gene Symbol FGFR3 [HGNC](#)
Chromosomal Location 4p16.3
UniGene ID Hs.1420 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000068078 [Ensembl](#)
LocusLink 2261 [NCBI](#)
P22607 [EMBL-EBI](#)

SwissProt	Q96T34	EMBL-EBI
	Q96T35	EMBL-EBI
	Q96T36	EMBL-EBI
	Q9NRB6	EMBL-EBI
EC	2.7.1.112	
OMIM	134934 NCBI	
RefSeq Protein ID	NP_000133	NCBI
	NP_075254	NCBI
RefSeq	RefSeq Transcript ID	RefSeq Title
	NM_000142 NCBI	fibroblast growth factor receptor 3 isoform 1 precursor
	NM_022965 NCBI	fibroblast growth factor receptor 3 isoform 2 precursor

Functional Annotations

	ID	Title	Organism	Type
Ortholog	DROSGENOME1:143549_AT	breathless	Drosophila	Putative Ortholog
	RAE230A:1369373_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RAE230B:1384056_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RAE230B:1384829_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RG-U34B:RC_AA899336_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RG-U34C:RC_AI136304_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	RG-U34C:RC_AI145424_AT	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	MG-U74AV2:160919_R_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MG-U74AV2:162253_I_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOE430A:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOE430A:1425796_A_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MU11KSUBA:M81342_S_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430_2:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430_2:1425796_A_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430A_2:1421841_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	MOUSE430A_2:1425796_A_AT	fibroblast growth factor receptor 3	Mouse	Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
165	MAPKKK cascade	experimental evidence	QuickGO AmiGO
1501	skeletal development	predicted/computed	QuickGO AmiGO
7048	oncogenesis	experimental evidence	QuickGO AmiGO
7259	JAK-STAT cascade	experimental	QuickGO

	8543 FGF receptor signaling pathway	evidence experimental evidence	AmiGO QuickGO AmiGO
	GO Cellular Component (view graph)		
	ID	Description	Evidence
Gene Ontology	5887 integral to plasma membrane	experimental evidence	QuickGO AmiGO
	GO Molecular Function (view graph)		
	ID	Description	Evidence
	5007 fibroblast growth factor receptor activity	experimental evidence	QuickGO AmiGO
Protein Similarities	Method	ID	Description
	blast	13112048	fibroblast growth factor receptor 3 isoform 2 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4 [Homo sapiens]
	blast	13186255	fibroblast growth factor receptor 2 isoform 3 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase [Homo sapiens]
	blast	4503711	fibroblast growth factor receptor 3 isoform 1 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4 [Homo sapiens]
	blast	20452380	
Protein Families	Method	ID	Description
	Hanks	FGFR-3	FGR3_HUMAN (FGFR-3) KINASES:5.6.3 PTK Group B membrane spanning protein tyrosine kinases.PTK XV Fibroblast growth factor receptor family .FGFR-3
	ec	ZA70_HUMAN	ZA70_HUMAN EC:2.7.1.112:TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KDA ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE).
	Hanks	FGFR-3	FGR3_HUMAN (FGFR-3) KINASES:5.6.3 PTK Group B membrane spanning protein tyrosine kinases.PTK XV Fibroblast growth factor receptor family .FGFR-3
	ec	ZA70_HUMAN	ZA70_HUMAN EC:2.7.1.112:TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KDA ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE).
	Database	ID	Description
	scop	d1gjoa_	d1gjoa_ SCOP:d.144.1.2: Fibroblast growth factor receptor 2
	scop	d1ev2e1	d1ev2e1 SCOP:b.1.1.4: Fibroblast growth factor receptor, FGFR
	scop	d1gjoa_	d1gjoa_ SCOP:d.144.1.2: Fibroblast growth factor receptor 2

Protein Domains	scop	<u>d1ev2e1</u>	d1ev2e1 SCOP:b.1.1.4: Fibroblast growth factor receptor, FGFR	4.25E-21
	pfam	<u>ig</u>	Immunoglobulin domain	1.6E-5
	pfam	<u>ig</u>	Immunoglobulin domain	3.2E-8
	pfam	<u>pkinase</u>	Protein kinase domain	2.3E-92
	pfam	<u>ig</u>	Immunoglobulin domain	1.6E-5
	pfam	<u>ig</u>	Immunoglobulin domain	3.2E-8
	pfam	<u>pkinase</u>	Protein kinase domain	2.3E-92
	pfam	<u>ig</u>	Immunoglobulin domain	7.3E-8
	InterPro	IPR000719 <u>EMBL-EBI</u>	Protein kinase	
	InterPro	IPR007110 <u>EMBL-EBI</u>	Immunoglobulin-like	
Protein Domains	InterPro	IPR001245 <u>EMBL-EBI</u>	Tyrosine protein kinase	
	InterPro	IPR008266 <u>EMBL-EBI</u>	Tyrosine protein kinase, active site	
	InterPro	IPR003598 <u>EMBL-EBI</u>	Immunoglobulin C-2 type	

Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000133	2	0.11005

Sequence

Target Sequence

>HUGENEFL:M64347_AT
gacttcaaagcaagctgggtattttcatatacaaatcttcttaattgctgtgtgtgtcccaggca
gggagacgggtttccagggaggggcccggccctgtgtgcagggttccgatgttattagatgtt
acaagtttatataatctatataataatttattgagtttttacaagatgtattgttgt
agacttaacacttcttacgcaatgcttcttagagttttatagcctggactgctacctttca
aagcttggaggaagccgtgaattcagttggttcggttctgtactgttactgggcccctgag
tctgggcagctgtcccttgcctgcagggccatggctcagggtggtctcttcttggg
gcccagtgcatggtggccagaggtgtcacccaaaccggcagggtgcgatt

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GACTTCAAAGCAAGCTGGTATTTTC	359	161	3348	Antisense
CATACAAATTCTTCTAATTGCTGTG	360	161	3372	Antisense
AATTCTTCTAATTGCTGTGTGTCCC	361	161	3378	Antisense
TGCTGTGTGTCCCAGGCAGGGAGAC	362	161	3390	Antisense
TGTGTGCAGGTTCCGATGTTATTAG	363	161	3438	Antisense
TCTTACGCAATGCTTCTAGAGTTTT	364	161	3540	Antisense
GCAATGCTTCTAGAGTTTTATAGCC	365	161	3546	Antisense
GAGTTTTATAGCCTGGACTGCTACC	366	161	3558	Antisense
TGCTACCTTTCAAAGCTTGGAGGGA	367	161	3576	Antisense
AAGCTTGGAGGGAAGCCGTGAATTC	368	161	3588	Antisense
TGAATTCAGTTGGTTCGTTCTGTAC	369	161	3606	Antisense
GTTTCGTTCTGTACTGTTACTGGGCC	370	161	3618	Antisense
CTGGGCCCTGAGTCTGGGCAGCTGT	371	161	3636	Antisense
CCTGAGTCTGGGCAGCTGTCCCTTG	372	161	3642	Antisense
TCTGGGCAGCTGTCCCTTGCTTGCC	373	161	3648	Antisense
TCCCTTGCTTGCCTGCAGGGCCATG	374	161	3660	Antisense

GCTTGCCTGCAGGGCCATGGCTCAG	375	161	3666	Antisense
CTTGGGGCCCAGTGCATGGTGGCCA	376	161	3702	Antisense
GTGGCCAGAGGTGTCACCCAAACCG	377	161	3720	Antisense
GTCACCCAAACCGGCAGGTGCGATT	378	161	3732	Antisense

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The Sequence Revision History tool allows you to see the various gi numbers, version numbers, and update dates for sequences that appeared in a specific GenBank record.

E.g., search for U46667 in the tool to see the old and current identifiers of the nucleotide sequence in that record.

Note that the original gi number for the nucleotide sequence, 2734632, does not have a corresponding version number. This is true because it was removed from the database (and replaced by 3172140) before the new accession.version system was implemented in Feb. 1999. At that time, each sequence in the GenBank/EMBL/DDBJ database received a version number of 1, even if they had been updated in the past.

In addition, if a GenBank record contains an updated sequence, the Comment field will contain a cross-reference to the gi number of the earlier sequence. (E.g., see U46667 in Entrez.) If you follow the link for that earlier gi number, Entrez will display that version of the GenBank record. Similarly, the Comment field of the older version will have a warning that the sequence has been updated, and will contain a cross-reference to the newer version.

More details about sequence identification numbers (GI and accession.version).

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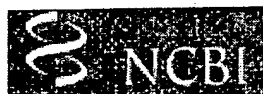
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Revised October 1, 2003

Questions about NCBI resources to info@ncbi.nlm.nih.gov

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PubMed

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Sequence Revision History

Find (Accessions, GI numbers or Fasta style SeqIds) U46667

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Revision history for U46667

GI	Version	Update Date	Status	I	II
3172140	1	<u>Aug 7 1998 9:28 AM</u>	Live	<input checked="" type="radio"/>	<input type="radio"/>
3172140	1	<u>Jun 2 1998 4:31 PM</u>	Dead	<input type="radio"/>	<input checked="" type="radio"/>
2734632	n/a	<u>Jan 3 1998 12:12 AM</u>	Dead	<input type="radio"/>	<input type="radio"/>
2734632	n/a	<u>Jan 1 1998 12:30 AM</u>	Dead	<input type="radio"/>	<input type="radio"/>

Accession U46667 was first seen at NCBI on Jan 1 1998 12:30 AM

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-> (0) All Descriptions
(L17131_rnal_at)
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(7129)

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Details for HUGENEFL:L17131_RNA1_AT

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GeneChip Array Information

Probe Set ID L17131_rna1_at
GeneChip Array HumanGeneFL Array
Organism Common Name Human

Probe Design Information

Transcript ID L17131_rna1
Sequence Type Exemplar sequence
Representative Public ID L17131 [NCBI](#)
Target Description L17131, class A, 20 probes, 20 in L17131mRNA#1 1646-2198, Human high mobility group protein (HMG-I(Y)) gene exons 1-8, complete cds

Sequence

>HUGENEFL:L17131_RNA1_AT
ttgtccaggtgaggcccaagagccctgtggccgccacctgaggtgggctggggctgtctcc
cctaaccctactttcgttccgccactcagccatttccccctcctcagatggggcaccaat
aacaaggagctcaccctgcccgcctcccaacccccctcctgtctcctccctgcccccaagg
ttctggttccatttttccctctgttcacaaactacctctggacagttgtgtgtttttgt
tcaatgttccattcttcgcacatccgtcattgtctgtctaccagcgccaaatgttcatcc
tcattgcctcctgttctgcccacgatccctcccccaagatactcttgtggggaagagg
ggctggggcatggcaggctgggtgaccgactacccagtcaccaggaaggtggggccctg
cccctaggatgctgcagcagagtgcagcaagggggcccgaaatcgaccataaagggtgtagg
ggccacctcctcccctgttctgttggggaggggtagccatgatttgtcccagcctgggg
ctccctctctggtttcctatttgcagttacttgaata

Target
Sequence

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
TTGTCCAGGTGAGGCCCAAGAGCCC	294	101	1658	Antisense
AGGTGAGGCCCAAGAGCCCTGTGGC	295	101	1664	Antisense
ACCAATAACAAGGAGCTCACCTGTC	296	101	1772	Antisense
TTTTCTCTGTTCAAACTACCTC	297	101	1850	Antisense
CTACCTCTGGACAGTTGTGTTGTTT	298	101	1868	Antisense
TTCCATTCTTCGACATCCGTCATTG	299	101	1904	Antisense
TCTTCGACATCCGTCATTGCTGCTG	300	101	1910	Antisense

Probe Info	GCTACCAGCGCCAAATGTTCATCCT	301	101	1934	Antisense
	TCATCCTCATTGCCTCCTGTTCTGC	302	101	1952	Antisense
	TCATTGCCTCCTGTTCTGCCACGA	303	101	1958	Antisense
	AAGATACTCTTTGTGGGGAAGAGGG	304	101	1994	Antisense
	GCAGGCTGGGTGACCGACTACCCCA	305	101	2030	Antisense
	CCCCTAGGATGCTGCAGCAGAGTGA	306	101	2078	Antisense
	AGCAAGGGGGCCCGAATCGACCATA	307	101	2102	Antisense
	CGAATCGACCATAAAGGGTGTAGGG	308	101	2114	Antisense
	GCCATGATTTGTCCCAGCCTGGGGC	309	101	2174	Antisense
	CTGGGGCTCCCTCTCTGGTTTCCTA	310	101	2192	Antisense
	CTCCCTCTCTGGTTTCCTATTTGCA	311	101	2198	Antisense
	CTCTGGTTTCCTATTTGCAGTTACT	312	101	2204	Antisense
	TTTCCTATTTGCAGTTACTTGAATA	313	101	2210	Antisense

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(L17131)
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Full Record**Details for HUGENEFL:X74801_AT****Full Screen**

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GeneChip Array Information

Probe Set ID X74801_at
**GeneChip
Array** HumanGeneFL Array
**Organism
Common
Name** Human

Probe Design Information

Transcript ID X74801
**Sequence
Type** Exemplar sequence
**Representative
Public ID** X74801 [NCBI](#)
**Target
Description** X74801, class B, 20 probes, 12 in X74801cds 1282-1552: 8 in reverseSequence,
1636-1837, H.sapiens Cctg mRNA for chaperonin

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)

Alignment(s)	Position	% Identity	Cytoband
chr1: 153495555-153497649 (-) UCSC		100	q22

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_005998 NCBI	chaperonin containing TCP1, subunit 3 (gamma)	chr1:153495551-153524840 (-) UCSC

Public Domain and Genome References

Gene Title chaperonin containing TCP1, subunit 3 (gamma)
Gene Symbol CCT3 [HGNC](#)
**Chromosomal
Location** 1q23
UniGene ID Hs.1708 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000163468 [Ensembl](#)
LocusLink 7203 [NCBI](#)
SwissProt AAH06501 [EMBL-EBI](#)
P49368 [EMBL-EBI](#)
OMIM 600114 [NCBI](#)
**RefSeq Protein
ID** NP_005989 [NCBI](#)

RefSeq RefSeq Transcript ID RefSeq Title
 NM_005998 NCBI chaperonin containing TCP1, subunit 3 (gamma)

Functional Annotations

	ID	Title	Organism	Type
	<u>ATH1-121501:246830_AT</u>	chaperonin, putative	Arabidopsis	Putative Ortholog
	<u>ATGENOME1:18906_AT</u>	chaperonin, putative	Arabidopsis	Putative Ortholog
	<u>DROSGENOME1:153982_AT</u>		Drosophila	Putative Ortholog
	<u>MG-U74AV2:161238_F_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MG-U74AV2:98153_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MG-U74CV2:171548_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1416024_X_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1426067_X_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1448178_A_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1449645_S_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1451915_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOE430A:1459987_S_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
Ortholog	<u>MU11KSUBA:C79428_RC_F_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MU11KSUBA:L20509_F_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430_2:1416024_X_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430_2:1426067_X_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430_2:1448178_A_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430_2:1449645_S_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430_2:1451915_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430_2:1459987_S_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A_2:1416024_X_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A_2:1426067_X_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A_2:1448178_A_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A_2:1449645_S_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog
	<u>MOUSE430A_2:1451915_AT</u>	chaperonin subunit 3 (gamma)	Mouse	Curated Ortholog

MOUSE430A 2:1459987 S AT chaperonin subunit 3 Mouse
(gamma) Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
6457	protein folding	traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5829	cytosol	not recorded	QuickGO AmiGO
5856	cytoskeleton	traceable author statement	QuickGO AmiGO

Gene Ontology

GO Molecular Function (view graph)

ID	Description	Evidence	Links
3754	chaperone activity	traceable author statement	QuickGO AmiGO
5524	ATP binding	inferred from electronic annotation	QuickGO AmiGO

Method	ID	Description	E-Value
blast	33873532		0.0
blast	31542292	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring complex, polypeptide 5 [Homo sapiens]	0.0

Protein Similarities

Database	ID	Description	E-Value
scop	d1a6da3	d1a6da3 SCOP:d.56.1.2: Thermosome	4.08E-25
scop	d1gmla	d1gmla_ SCOP:c.8.5.2: Thermosome	1.01E-57
scop	d1a6da1	d1a6da1 SCOP:a.129.1.2: Thermosome	4.81E-83
pfam	cpn60_TCP1	TCP-1/cpn60 chaperonin family	5.7E-210
InterPro	IPR002423 EMBL-EBI	Chaperonin Cpn60/TCP-1	
InterPro	IPR001844 EMBL-EBI	Chaperonin Cpn60	
InterPro	IPR002194 EMBL-EBI	Chaperonin TCP-1	
InterPro	IPR008950 EMBL-EBI	GroEL-like chaperone, ATPase	

Protein Domains

Sequence

>HUGENEFL:X74801_AT
atgactggtgtggaacaatggccatacagggtgtgtgccaggccctagaggtcatttcct
cgtaccctgatccagaactgtggggccagcaccatccgtctacttacctcccttcggggcc
aagcacacccaggagaactgtgagacctgggggtgtaaattggtgagacgggtactttggtg
gacatgaaggaactgggcataatgggagccattggctgtgaagctgcagacttataagaca
gcagtggagacggcagttctgctactgccaattgatgacatcgtttcaggccacaaaag
aaaggcgatgaccagagccggcaaggcggggtcctgatgctggccaggagtgagtgtta
ggcaaggctacttcaatgcacagaaaccagcagagtcctcccttttcctgagccagagtgc
caggaacactgtggcagctctttgttcagaagggatcaggttggggggcagcccccagtc
ctttctgtccagctcagttttccaaaagacactgacatgtaattcttctctattgttaag
gtttccatttagtttgcctccgatgattaaatctaagtca

Target Sequence

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
-----------------------	---------	---------	------------------------------	--------------

Probe Info	ATGACTGGTGTGGAACAATGGCCAT	60	345	1294	Antisense
	GAACAATGGCCATACAGGGCTGTTG	61	345	1306	Antisense
	CTGATCCAGAACTGTGGGGCCAGCA	62	345	1360	Antisense
	CAGAACTGTGGGGCCAGCACCATCC	63	345	1366	Antisense
	TGTGGGGCCAGCACCATCCGTCTAC	64	345	1372	Antisense
	CTGGGCATATGGGAGCCATTGGCTG	65	345	1486	Antisense
	ATATGGGAGCCATTGGCTGTGAAGC	66	345	1492	Antisense
	GAGCCATTGGCTGTGAAGCTGCAGA	67	345	1498	Antisense
	TTGGCTGTGAAGCTGCAGACTTATA	68	345	1504	Antisense
	GAGACGGCAGTTCTGCTACTGCGAA	69	345	1540	Antisense
	GCAGTTCTGCTACTGCGAATTGATG	70	345	1546	Antisense
	ATTGATGACATCGTTTCAGGCCACA	71	345	1564	Antisense
	GTGCTAGGCAAGGCTACTTCAATGC	72	345	1648	Antisense
	GGCAAGGCTACTTCAATGCACAGAA	73	345	1654	Antisense
	GCTACTTCAATGCACAGAACCAGCA	74	345	1660	Antisense
	CACAGAACCAGCAGAGTCTCCCCTT	75	345	1672	Antisense
	GAGCCAGAGTGCCAGGAACACTGTG	76	345	1702	Antisense
	CACTGACATGTAATTCTTCTCTATT	77	345	1804	Antisense
	TAGTTTGCTTCCGATGATTAAATCT	78	345	1843	Antisense
	GCTTCCGATGATTAAATCTAAGTCA	79	345	1849	Antisense

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Details for HUGENEFL:U15008_AT
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NetAffx Links [Cluster Members](#)
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GeneChip Array Information

Probe Set ID U15008_at
GeneChip Array HumanGeneFL Array
Organism Common Name Human

Probe Design Information

Transcript ID U15008
Sequence Type Exemplar sequence
Representative Public ID U15008 [NCBI](#)
Target U15008, class A, 20 probes, 20 in U15008 25-433, Human SnRNP core protein
Description Sm D2 mRNA, complete cds

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)
Alignment(s) Position % Identity Cytoband
chr19: 50882580-50883664 (-) [UCSC](#) 98 q13.32

Representative Transcript	UniGene Description	Position
NM_004597 NCBI	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	chr19:50882558-50887282 (-) UCSC
NM_177542 NCBI	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	chr19:50882558-50887282 (-) UCSC

Public Domain and Genome References

Gene Title small nuclear ribonucleoprotein D2 polypeptide 16.5kDa
Gene Symbol SNRPD2 [HGNC](#)
Chromosomal Location 19q13.2
UniGene ID Hs.424327 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000125743 [Ensembl](#)
LocusLink 6633 [NCBI](#)
SwissProt P43330 [EMBL-EBI](#)
OMIM 601061 [NCBI](#)

RefSeq Protein ID	NP_004588 NCBI
	NP_808210 NCBI
RefSeq Transcript ID	RefSeq Title
RefSeq	NM_004597 NCBI small nuclear ribonucleoprotein polypeptide D2
	NM_177542 NCBI small nuclear ribonucleoprotein polypeptide D2

Functional Annotations

	ID	Title	Organism	Type
	ATH1-121501:266482_AT	small nuclear ribonucleo protein D2 -related	Arabidopsis	Putative Ortholog
	C. ELEGANS:172931_X_AT	small nuclear ribonucleoprotein D2 like	Celegans	Putative Ortholog
	DROSGENOME1:153483_AT		Drosophila	Putative Ortholog
Ortholog	MG-U74AV2:95049_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	MOE430A:1452680_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	MU11KSUBA:AA271024_S_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	MOUSE430_2:1452680_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog
	MOUSE430A_2:1452680_AT	small nuclear ribonucleoprotein D2	Mouse	Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
245	spliceosome assembly	traceable author statement	QuickGO AmiGO
6371	mRNA splicing	traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

	ID	Description	Evidence	Links
Gene Ontology	5681	spliceosome complex	traceable author statement	QuickGO AmiGO
	5732	small nucleolar ribonucleoprotein complex	inferred from electronic annotation	QuickGO AmiGO
	30532	small nuclear ribonucleoprotein complex	traceable author statement	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
8248	pre-mRNA splicing factor activity	inferred from electronic annotation	QuickGO AmiGO

	Method	ID	Description	E-Value
Protein Similarities	blast	4759158	small nuclear ribonucleoprotein polypeptide D2; snRNP core protein D2 [Homo sapiens]	1.0E-62
	blast	26337731		3.0E-62
	blast	4759158	small nuclear ribonucleoprotein polypeptide D2; snRNP core protein D2 [Homo sapiens]	1.0E-62
	blast	26337731		3.0E-62

Database	ID	Description	E-Value
scop	d1b34b	d1b34b_SCOP:b.38.1.1: D2 core SNRNP	1.85E-

Protein Domains	scop	d1b34b	protein	28
			d1b34b_SCOP:b.38.1.1; D2 core SNRNP	1.85E-28
	pfam	LSM	LSM domain	1.1E-16
	pfam	LSM	LSM domain	1.1E-16
	InterPro	IPR001163	Small nuclear ribonucleoprotein (Sm protein)	
		EMBL-EBI		

Sequence

>HUGENEFL:U15008_AT
 accatcatgagcctcctcaacaagcccaagagtgagatgacccagaggagctgcagaag
 cgagaggaggaggaatttaacaccggtccactctctgtgctcacacagtcagtcagaac
 aatacccaagtgtcatcaactgccgaacaataagaaactcctggcgcggtgaaggcc
 ttcgataggcactgcaacatggtgctggagaacgtgaaggagatgtggactgaggtacc
 aagagtggcaagggaagaagaagtccaagccagtcaacaaagaccgctacatctccaag
 atgttcctgcgcggggactcagtcacgtggtcctgcggaaccgctcatcgccggcaag
 tagggcgccgtgtctgttgacagaactcactcctctgtcctatgaagaccgctgccatt
 ggtgttgagaata

Probe Info	Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
	ACCATCATGAGCCTCCTCAACAAGC	99	211	37	Antisense
	AGTGAGATGACCCCAGAGGAGCTGC	100	211	67	Antisense
	AACACCGGTCCACTCTCTGTGCTCA	101	211	115	Antisense
	GGTCCACTCTCTGTGCTCACACAGT	102	211	121	Antisense
	CTCTCTGTGCTCACACAGTCAGTCA	103	211	127	Antisense
	GTGCTCACACAGTCAGTCAAGAACA	104	211	133	Antisense
	TCAGTCAAGAACAATACCCAAGTGC	105	211	145	Antisense
	AATACCCAAGTGCTCATCAACTGCC	106	211	157	Antisense
	CAAGTGCTCATCAACTGCCGCAACA	107	211	163	Antisense
	CGCGTGAAGGCCTTCGATAGGCACT	108	211	205	Antisense
	AAGGCCTTCGATAGGCACTGCAACA	109	211	211	Antisense
	TTCGATAGGCACTGCAACATGGTGC	110	211	217	Antisense
	GTACCCAAGAGTGGCAAGGGCAAGA	111	211	271	Antisense
	TACATCTCCAAGATGTTCTGCGCG	112	211	325	Antisense
	TCAGTCATCGTGGTCCTGCGGAACC	113	211	355	Antisense
	TAGGGGCCGCCTGTCTGTTGACAGA	114	211	397	Antisense
	TGACAGAACTCACTCCTCTGTCTTA	115	211	415	Antisense
	CTCCTCTGTCTATGAAGACCGCTG	116	211	427	Antisense
	TGTCCTATGAAGACCGCTGCCATTG	117	211	433	Antisense
	ACCGCTGCCATTGGTGTGAGAATA	118	211	445	Antisense

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Details for HUGENEFL:AFFX-BIOB-M_ST

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GeneChip Array Information

Probe Set ID: AFFX-BioB-M_st
 GeneChip Array: HumanGeneFL Array
 Organism Common Name: Human

Probe Design Information

Transcript ID: AFFX-BioB-M
 Sequence Type: Control sequence
 Representative Public ID: J04423 [NCBI](#)
 Target Description: J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

Sequence

>HUGENEFL:AFFX-BIOB-M_ST
 gccggagttttacggcaatatcatcaccacacgcacttatcaggaacgcctcgatacgc
 ggaaaaagtgcgcgatgccgggatacaagtcgttctggcggcatttgtgggcttaggcga
 aacggtaaaagatcgccgcgattattgctgcaactggcaaacctgccgacgcgcgcgga
 aagcgtgccaatcaacatgctggtgaaggtgaaaggcacgcgcgcttgccgataacgatga
 tgcgatgcctttgatatt

Target Sequence

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GATGATATTGCCGTA AAACTCCGGC	201	11	483	Sense
TGTGGTGATGATATTGCCGTA AAC	202	11	489	Sense
TAAGTGCGTGTGGTGATGATATTGC	203	11	497	Sense
GTTCTGTATAAGTGCGTGTGGTGAT	204	11	505	Sense
ATCGAGGCGTTCTGTATAAGTGCGT	205	11	513	Sense
GCATCGCGCACTTTTCCAGCGTAT	206	11	536	Sense
GATCCCGGCATCGCGCACTTTTCC	207	11	543	Sense
GACTTTGATCCCGGCATCGCGCACT	208	11	549	Sense
CGCCAGAACAGACTTTGATCCCGGC	209	11	559	Sense
CCCACAATGCCGCCAGAACAGACTT	210	11	569	Sense

TGCAGCAATAATCCGGCGCGATCTT	211	11	611	Sense
TTGCCAGTTGCAGCAATAATCCGGC	212	11	619	Sense
CGGCAGGTTTGCCAGTTGCAGCAAT	213	11	627	Sense
ATGTTGATTGGCACGCTTTCGGCG	214	11	656	Sense
CACCAGCATGTTGATTGGCACGCTT	215	11	663	Sense
TTCACCTTCACCAGCATGTTGATTG	216	11	671	Sense
AGCGGCGTGCCTTTCACCTTCACCA	217	11	683	Sense
CATCATCGTTATCGGCAAGCGGCGT	218	11	700	Sense
GCATCGACATCATCGTTATCGGCAA	219	11	707	Sense
AAATCAAAGGCATCGACATCATCGT	220	11	716	Sense

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Details for HUGENEFL:AFFX-BIODN-5_ST

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GeneChip Array Information

Probe Set ID AFFX-BioDn-5_st
 GeneChip Array HumanGeneFL Array
 Organism Common Name Human

Probe Design Information

Transcript ID AFFX-BioDn-5
 Sequence Type Control sequence
 Representative Public ID J04423 [NCBI](#)
 Target Description J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

Sequence

Target Sequence

>HUGENEFL:AFFX-BIODN-5_ST
 gggaaaactgtcgccagttgtgcacttttacaagccgcaaaggcagcaggctaccggagc
 gcaggttataaacgggtcgccctctggcagcgaaaagaccccggaaggtttacgcaatagc
 gacgcgctggcggttacagcgcaacagcagcctgcagctggattacgcaacagtaaatcct
 tacaccttcgcagaaccacttcgcgcacatcatcagcgcgcaagagggcagaccgata
 gaatcattggtaatgagcgccggattacgcgcgcttg

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
GTGCACAACTGGCGACAGTTTCCC	281	11	49	Sense
GGCTTGTAAGTGCACAACTGGCG	282	11	60	Sense
GCTGCCTTTGCGGCTTGTAAGT	283	11	71	Sense
GGTAGCCTGCTGCCTTTGCGGCTTG	284	11	79	Sense
CCGTCGCGTAGCCTGCTGCCTTTGC	285	11	85	Sense
CAGCGCGTCGCTATTGCGTAAACCT	286	11	153	Sense
GTAACGCCAGCGCGTCGCTATTGCG	287	11	160	Sense
TTGCGCTGTAACGCCAGCGCGTCGC	288	11	167	Sense
TGCTGTTGCGCTGTAACGCCAGCGC	289	11	172	Sense
TGCAGGCTGCTGTTGCGCTGTAACG	290	11	179	Sense

TCCAGCTGCAGGCTGCTGTTGCGCT	291	11	185	Sense
TGCGTAATCCAGCTGCAGGCTGCTG	292	11	192	Sense
TTACTGTTGCGTAATCCAGCTGCAG	293	11	199	Sense
CGGTCTGCCCTCTTGCGCGCTGATG	294	11	261	Sense
GATTCTATCGGTCTGCCCTCTTGCG	295	11	269	Sense
TACCAATGATTCTATCGGTCTGCCC	296	11	276	Sense
CTCATTACCAATGATTCTATCGGTC	297	11	281	Sense
TCCGGCGCTCATTACCAATGATTCT	298	11	288	Sense
CGCGTAATCCGGCGCTCATTACCAA	299	11	295	Sense
CAAGCGCGCGTAATCCGGCGCTCAT	300	11	301	Sense

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HT4804_s_at)
-> (1) All Descriptions
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5_st)
-> (1) All Descriptions
(AFFX-BioB-M_st)
-> (1) All Descriptions
(HG613)

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Details for HUGENEFL:X15880_AT

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GeneChip Array Information

Probe Set ID X15880_at
**GeneChip
Array** HumanGeneFL Array
**Organism
Common
Name** Human

Probe Design Information

Transcript ID X15880
**Sequence
Type** Exemplar sequence
**Representative
Public ID** X15880 [NCBI](#)
**Target
Description** X15880, class C, 20 probes; 20 in all_X15880 1690-2273, Human mRNA for collagen VI alpha-1 C-terminal globular domain

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)

Alignment(s)	Position	% Identity	Cytoband
chr21: 46280561-46281145 (+) UCSC		100	q22.3

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_001848 NCBI	collagen, type VI, alpha 1	chr21:46257869-46281164 (+) UCSC

Public Domain and Genome References

Gene Title collagen, type VI, alpha 1
Gene Symbol COL6A1 [HGNC](#)
**Chromosomal
Location** 21q22.3
UniGene ID Hs.415997 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000142156 [Ensembl](#)
LocusLink 1291 [NCBI](#)
SwissProt P12109 [EMBL-EBI](#)
Q7Z645 [EMBL-EBI](#)
Q8TBN2 [EMBL-EBI](#)
Q9BSA8 [EMBL-EBI](#)
OMIM 120220 [NCBI](#)

RefSeq Protein ID NP_001839 NCBI

RefSeq Transcript ID RefSeq Title
NM_001848 NCBI collagen, type VI, alpha 1 precursor

Functional Annotations

	ID	Title	Organism	Type
Ortholog	MG-U74AV2:162459_F_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MG-U74AV2:95493_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MOE430A:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MU11KSUBB:X66405_S_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MOUSE430_2:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog
	MOUSE430A_2:1448590_AT	procollagen, type VI, alpha 1	Mouse	Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
7155	cell adhesion	non-traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5578	extracellular matrix	inferred from electronic annotation	QuickGO AmiGO
5589	collagen type VI	non-traceable author statement	QuickGO AmiGO

Gene Ontology

GO Molecular Function (view graph)

ID	Description	Evidence	Links
5194	cell adhesion molecule activity	inferred from electronic annotation	QuickGO AmiGO
5201	extracellular matrix structural constituent	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities

Method	ID	Description	E-Value
blast	15011913		0.0
blast	13878903		0.0

Protein Domains

Database	ID	Description	E-Value
scop	d1atza_	d1atza_SCOP:c.62.1.1: von Willebrand factor A3 domain	3.63E-37
pfam	vwa	von Willebrand factor type A domain	9.6E-24
pfam	vwa	von Willebrand factor type A domain	4.7E-32
pfam	vwa	von Willebrand factor type A domain	2.7E-35
pfam	Collagen	Collagen triple helix repeat (20 copies)	2.4E-11
pfam	Collagen	Collagen triple helix repeat (20 copies)	3.8E-14
pfam	Collagen	Collagen triple helix repeat (20 copies)	3.3E-10
pfam	Collagen	Collagen triple helix repeat (20 copies)	2.6E-11
InterPro	IPR008161 EMBL-EBI	Collagen helix repeat	
InterPro	IPR002035 EMBL-EBI	von Willebrand factor, type A	

InterPro IPR008160 Collagen triple helix repeat
EMBL-EBI

Sequence

>HUGENEFL:X15880_AT

agcaagacgcctctcggggcctgtgccgcactagcctccctctcctctgtcccatagct
 ggtttttcccaaatcctcacctaacagttactttacaattaaactcaaagcaagctct
 tctcctcagcttggggcagccattggcctctgtctcgttttgggaaccaaggtcaggag
 gccgttgacagacataaatctcggcgactcggccccgtctcctgagggctcctgctggtgac
 cggcctggaccttggccctacagccctggaggccgctgctgaccagcactgaccccgacc
 tcagagagtactcgcagggcgctggctgcactcaagaccctcgagattaacggtgctaa
 ccccgctctgctcctccctcccgacagagactggggcctggactggacatgagagcccttg
 gtgccacagagggctgtgtcttactagaaacaacgcaaacctctcctcctcagaatagt
 gatgtgttcgacgttttatcaaaggccccctttctatgttcatgttagtttgccttc
 tgtgtttttttctgaaccatatccatgttgctgacttttccaa

Target
 Sequence

Probe Info	Probe Sequence(5'-3')	Probe		Probe Interrogation Position	Strandedness
		X	Y		
	AGCAAGACGCCTCTCGGGGCCTGTG	76	317	1702	Antisense
	AAACTCAAAGCAAGCTCTTCTCCTC	77	317	1804	Antisense
	AAAGCAAGCTCTTCTCCTCAGCTTG	78	317	1810	Antisense
	TCTCCTCAGCTTGGGGCAGCCATTG	79	317	1822	Antisense
	GCCATTGGCCTCTGTCTCGTTTTGG	80	317	1840	Antisense
	GCAGACATAAATCTCGGCGACTCGG	81	317	1888	Antisense
	GCCCCGTCTCCTGAGGGTCTGCTG	82	317	1912	Antisense
	TGGCCCTACAGCCCTGGAGGCCGCT	83	317	1954	Antisense
	TCAGAGAGTACTCGCAGGGGCGCTG	84	317	2002	Antisense
	AGTACTCGCAGGGGCGCTGGCTGCA	85	317	2008	Antisense
	GGCGCTGGCTGCACTCAAGACCCTC	86	317	2020	Antisense
	GGACATGAGAGCCCCTTGGTGCCAC	87	317	2104	Antisense
	GAGAGCCCCTTGGTGCCACAGAGGG	88	317	2110	Antisense
	CCCTTGGTGCCACAGAGGGCTGTGT	89	317	2116	Antisense
	GTGCCACAGAGGGCTGTGTCTTACT	90	317	2122	Antisense
	CAGAGGGCTGTGTCTTACTAGAAAC	91	317	2128	Antisense
	CTCCTTCCTCAGAATAGTGATGTGT	92	317	2164	Antisense
	TTTTTCTGAACCATATCCATGTTGC	93	317	2248	Antisense
	TGAACCATATCCATGTTGCTGACTT	94	317	2254	Antisense
	ATATCCATGTTGCTGACTTTTCCAA	95	317	2260	Antisense

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GeneChip Array Information
Probe Set ID U23752_at
**GeneChip
Array** HumanGeneFL Array
**Organism
Common
Name** Human

Probe Design Information
Transcript ID U23752
**Sequence
Type** Exemplar sequence
**Representative
Public ID** U23752 [NCBI](#)
Target U23752, class A, 20 probes, 20 in U23752 1679-1919, Human SOX-11 mRNA,
Description complete cds

Genomic Alignment of Target Sequence
Assembly April 2003 (NCBI 33)

Alignment(s)	Position	% Identity	Cytoband
chr2: 5856192-5856457 (+) UCSC	99	p25.2	

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_003108 NCBI	SRY (sex determining region Y)- box 11	chr2:5854537-5863255 (+) UCSC

Public Domain and Genome References
Gene Title SRY (sex determining region Y)-box 11
Gene Symbol SOX11 [HGNC](#)
**Chromosomal
Location** 2p25
UniGene ID Hs.432638 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000176887 [Ensembl](#)
LocusLink 6664 [NCBI](#)
SwissProt P35716 [EMBL-EBI](#)
OMIM 600898 [NCBI](#)
**RefSeq Protein
ID** NP_003099 [NCBI](#)

RefSeq Transcript ID RefSeq Title
 NM_003108 [NCBI](#) SRY-box 11

Functional Annotations

	ID	Title	Organism	Type
Ortholog	RAE230A:1387275_AT	SRY-box containing gene 11	Rat	Putative Ortholog
	RG-U34A:AJ004858_AT	SRY-box containing gene 11	Rat	Putative Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
6355	regulation of transcription, DNA-dependent	inferred from electronic annotation	QuickGO AmiGO
7399	neurogenesis	traceable author statement	QuickGO AmiGO

Gene Ontology

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5634	nucleus	inferred from electronic annotation	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
3677	DNA binding	inferred from electronic annotation	QuickGO AmiGO

Method	ID	Description	E-Value
blast	4507161	SRY-box 11; SRY (sex-determining region Y)-box 11; SRY-related HMG-box gene 11; transcription factor SOX-11 [Homo sapiens]	0.0
blast	23831472		0.0

Protein Similarities

Database	ID	Description	E-Value
scop	d1i11a	d1i11a_ SCOP:a.21.1.1: Sox-5	2.36E-19
pfam	HMG_box	HMG (high mobility group) box	1.1E-33
InterPro	IPR000910	HMG1/2 (high mobility group) box	
	EMBL-EBI		

Protein Domains

Sequence

Target Sequence

>HUGENEFL:U23752_AT
 cttcctttatcgtgtctcaaggtagttgcatacctagtctggagttgtgattatntttccc
 aaaaaatgtgtttttgtaattactattttctttttcctgaaattcgtgattgcaacaaagg
 cagagggggcgggcgggcgaggaggtaggaccgctccggaaggcgctgtttgaagc
 ttgtcggctcttgaagtctggaagacgtctgcagaggaccttttggcagcacaaactgtt
 actctagggagttggtggagatatt

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
CTTCCTTTATCGTGTCTCAAGGTAG	503	219	1691	Antisense
TTATCGTGTCTCAAGGTAGTTGCAT	504	219	1697	Antisense
TCGTGTCTCAAGGTAGTTGCATACC	505	219	1700	Antisense
AAGGTAGTTGCATACCTAGTCTGGA	506	219	1709	Antisense
GTAGTTGCATACCTAGTCTGGAGTT	507	219	1712	Antisense

	GTTGCATACCTAGTCTGGAGTTGTG	508	219	1715	Antisense
	TACCTAGTCTGGAGTTGTGATTATT	509	219	1721	Antisense
	CTAGTCTGGAGTTGTGATTATTTTC	510	219	1724	Antisense
	TGTGATTATTTTCCCAAAAATGTG	511	219	1736	Antisense
	TTTTCTGAAATTCGTGATTGCAAC	512	219	1781	Antisense
	GCTCCGGAAGGCGCTGTTTGAAGCT	513	219	1847	Antisense
	GCTGTTTGAAGCTTGTCTGGTCTTTG	514	219	1859	Antisense
Probe Info	TGAAGCTTGTCTGGTCTTTGAAGTCT	515	219	1865	Antisense
	TTGTCTGGTCTTTGAAGTCTGGAAGA	516	219	1871	Antisense
	TGGAAGACGTCTGCAGAGGACCCTT	517	219	1889	Antisense
	AAGACGTCTGCAGAGGACCCTTTTG	518	219	1892	Antisense
	GCAGAGGACCCTTTTGGCAGCACAA	519	219	1901	Antisense
	AGCACAACTGTTACTCTAGGGAGTT	520	219	1919	Antisense
	ACTGTTACTCTAGGGAGTTGGTGGA	521	219	1925	Antisense
	ACTCTAGGGAGTTGGTGGAGATATT	522	219	1931	Antisense

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Full Record

Details for HUGENEFL:M12625_AT

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GeneChip Array Information

Probe Set ID M12625_at
 GeneChip HumanGeneFL Array
 Array
 Organism Human
 Common
 Name

Probe Design Information

Transcript ID M12625
 Sequence Exemplar sequence
 Type
 Representative M12625 [NCBI](#)
 Public ID
 Target
 Description M12625, class B, 20 probes, 13 in M12625mRNA 893-1259: 7 in
 reverseSequence, 1599-1683, Human lecithin-cholesterol acyltransferase mRNA,
 complete cds, with 5' and 3' flanking DNA sequences

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)
 Alignment(s) Position % Identity Cytoband
 chr16: 67749925-67750484 (-) [UCSC](#) 100 q22.1

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
M12625 NCBI	lecithin-cholesterol acyltransferase	chr16:67749888-67754507 (-) UCSC	

Public Domain and Genome References

Gene Title lecithin-cholesterol acyltransferase
 Gene Symbol LCAT [HGNC](#)
 Chromosomal 16q22.1
 Location
 UniGene ID Hs.387239 [NCBI](#) (FULL LENGTH)
 Ensembl ENSG00000103080 [Ensembl](#)
 LocusLink 3931 [NCBI](#)
 SwissProt AAP88750 [EMBL-EBI](#)
 P04180 [EMBL-EBI](#)
 EC 2.3.1.43
 OMIM 606967 [NCBI](#)

RefSeq Protein ID NP_000220 [NCBI](#)

RefSeq RefSeq Transcript ID RefSeq Title
NM_000229 [NCBI](#) lecithin-cholesterol acyltransferase precursor

Functional Annotations

	ID	Title	Organism	Type
Ortholog	MG-U74AV2:103023 AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	MG-U74AV2:161759 R AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	MOE430A:1417043 AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	MU11KSUBA:J05154 S AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	RAE230A:1367887 AT	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
	RG-U34A:X54096 AT	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
	MOUSE430 2:1417043 AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
	MOUSE430A 2:1417043 AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
6629	lipid metabolism	inferred from electronic annotation	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5576	extracellular	not recorded	QuickGO AmiGO

Gene Ontology

GO Molecular Function (view graph)

ID	Description	Evidence	Links
4607	phosphatidylcholine-sterol O-acyltransferase activity	inferred from electronic annotation	QuickGO AmiGO
8415	acyltransferase activity	inferred from electronic annotation	QuickGO AmiGO
16740	transferase activity	inferred from electronic annotation	QuickGO AmiGO

	Method	ID	Description	E-Value
Protein Similarities	blast	32879837		0.0
	blast	4557892	lecithin-cholesterol acyltransferase precursor [Homo sapiens]	0.0

	Method	ID	Description	E-Value
Protein Families	ec	LCAT_HUMAN	LCAT_HUMAN	1.85E-171
			EC:2.3.1.43:PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE).	

Database	ID	Description	E-Value
----------	----	-------------	---------

scop [d1tca](#) d1tca__ SCOP:c.69.1.17:| Triacylglycerol lipase 5.3E-8
 pfam [LACT](#) Lecithin:cholesterol acyltransferase 1.7E-182

InterPro IPR003386 Lecithin:cholesterol acyltransferase
[EMBL-EBI](#)

Protein Domains InterPro IPR008262 Lipase, active site
[EMBL-EBI](#)

Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000220	2	0.05945

Sequence

>HUGENEFL:M12625_AT
 cttcaactacacaggccgtgacttccaacgcttctttgcagacctgcactttgaggaagg
 ctggtacatgtggctgcagtcacgtgacctcctggcaggactcccagcacctgggtgga
 agtatactgtctttacggcggtgggctgcccacgccccgcacctacatctacgaccacgg
 cttccctacacggacctgtgggtgtgctctatgaggatggatgacacgggtggcgac
 ccgcagcaccgagctctgtggcctgtggcaggccgcagccacagcctgtgcacctgct
 gccctgcacgggatacagcatctcaacatgggtcttcagcaacctgacctggagcacat
 caatgccatcctgtgggtgcctaccgccagggtccccctgcacccccgactgccagccc
 agagccccgcctcctgaataaagaccttctttgtaccgtaagccctgatggctatgt
 ttcaggttgaaggaggcactagagtcacacactaggtttcactcctcaccagccacagg
 ctgagtgctgtgtgcagtg

Target Sequence

Probe Info	Probe Sequence(5'-3')	Probe		Probe Interrogation Position	Strandedness
		X	Y		
	CTTCAACTACACAGGCCGTGACTTC	152	127	1161	Antisense
	CTACACAGGCCGTGACTTCCAACGC	153	127	1167	Antisense
	CCAACGCTTCTTTGCAGACCTGCAC	154	127	1185	Antisense
	CCTGCACTTTGAGGAAGGCTGGTAC	155	127	1203	Antisense
	CATGTGGCTGCAGTCACGTGACCTC	156	127	1227	Antisense
	GCTGCAGTCACGTGACCTCCTGGCA	157	127	1233	Antisense
	CCTGGCAGGACTCCAGCACCTGGT	158	127	1251	Antisense
	GGACCCTGTGGGTGTGCTCTATGAG	159	127	1353	Antisense
	TGTGCTCTATGAGGATGGTGATGAC	160	127	1365	Antisense
	GGCGACCCGCAGCACCGAGCTCTGT	161	127	1395	Antisense
	CCTGACCCTGGAGCACATCAATGCC	162	127	1503	Antisense
	GCACATCAATGCCATCCTGCTGGGT	163	127	1515	Antisense
	CATCCTGCTGGGTGCCTACCGCCAG	164	127	1527	Antisense
	CTTTGCTACCGTAAGCCCTGATGGC	165	127	1611	Antisense
	TACCGTAAGCCCTGATGGCTATGTT	166	127	1617	Antisense
	AAGCCCTGATGGCTATGTTTCAGGT	167	127	1623	Antisense
	CTATGTTTCAGGTTGAAGGGAGGCA	168	127	1635	Antisense
	GGAGGCACTAGAGTCCCACACTAGG	169	127	1653	Antisense
	GTCCCACACTAGGTTTCACTCCTCA	170	127	1665	Antisense
	CACAGGCTCAGTGCTGTGTGCAGTG	171	127	1695	Antisense

